

10/009330

1

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Screening Method Using CD100

5 <130> 2611W00P

<150> JP 11-157111

<151> 1999-06-03

<160> 10

<210> 1

10 <211> 861

<212> PRT

<213> Mouse

<400> 1

Met Arg Met Cys Ala Pro Val Arg Gly Leu Phe Leu Ala Leu Val Val

15 1 5 10 15

Val Leu Arg Thr Ala Val Ala Phe Ala Pro Val Pro Arg Leu Thr Trp

20 25 30

Glu His Gly Glu Val Gly Leu Val Gln Phe His Lys Pro Gly Ile Phe

35 40 45

20 Asn Tyr Ser Ala Leu Leu Met Ser Glu Asp Lys Asp Thr Leu Tyr Val

50 55 60

Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu

65 70 75 80

Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ser Lys

25 85 90 95

Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile

100 105 110

Arg Val Leu Gln Pro Leu Ser Ser Thr Ser Leu Tyr Val Cys Gly Thr

115 120 125

Asn Ala Phe Gln Pro Thr Cys Asp His Leu Asn Leu Thr Ser Phe Lys
 130 135 140
 Phe Leu Gly Lys Ser Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro
 145 150 155 160
 5 Ala His Ser Tyr Thr Ser Val Met Val Gly Gly Glu Leu Tyr Ser Gly
 165 170 175
 Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
 180 185 190
 Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu
 10 195 200 205
 Pro Ser Phe Val Phe Ala Asp Val Ile Gln Lys Ser Pro Asp Gly Pro
 210 215 220
 Glu Gly Glu Asp Asp Lys Val Tyr Phe Phe Phe Thr Glu Val Ser Val
 225 230 235 240
 15 Glu Tyr Glu Phe Val Phe Lys Leu Met Ile Pro Arg Val Ala Arg Val
 245 250 255
 Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr
 260 265 270
 Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Lys Pro Asp Ser Gly Leu
 20 275 280 285
 Val Phe Asn Ile Leu Gln Asp Val Phe Val Leu Arg Ala Pro Gly Leu
 290 295 300
 Lys Glu Pro Val Phe Tyr Ala Val Phe Thr Pro Gln Leu Asn Asn Val
 305 310 315 320
 25 Gly Leu Ser Ala Val Cys Ala Tyr Thr Leu Ala Thr Val Glu Ala Val
 325 330 335
 Phe Ser Arg Gly Lys Tyr Met Gln Ser Ala Thr Val Glu Gln Ser His
 340 345 350
 Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Thr Pro Arg Pro Gly

	355		360		365
	Ala Cys Ile Asp Ser Glu	Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu			
	370		375		380
	Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met				
5	385		390		395 400
	Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Lys Leu Ile Lys Lys				
		405		410	415
	Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp				
		420		425	430
10	Gly Thr Phe Tyr Asp Val Met Phe Ile Ser Thr Asp Arg Gly Ala Leu				
		435		440	445
	His Lys Ala Val Ile Leu Thr Lys Glu Val His Val Ile Glu Glu Thr				
		450		455	460
	Gln Leu Phe Arg Asp Phe Glu Pro Val Leu Thr Leu Leu Leu Ser Ser				
15	465		470		475 480
	Lys Lys Gly Arg Lys Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val				
		485		490	495
	Gln Ala Pro Leu Ala Phe Cys Glu Lys His Gly Ser Cys Glu Asp Cys				
		500		505	510
20	Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Ala Ile Lys Ala				
		515		520	525
	Cys Val Thr Leu His Gln Glu Glu Ala Ser Ser Arg Gly Trp Ile Gln				
		530		535	540
	Asp Met Ser Gly Asp Thr Ser Ser Cys Leu Asp Lys Ser Lys Glu Ser				
25	545		550		555 560
	Phe Asn Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys				
		565		570	575
	Phe Gln Lys Ser Asn Leu Ala Arg Val Val Trp Lys Phe Gln Asn Gly				
		580		585	590

	Glu	Leu	Lys	Ala	Ala	Ser	Pro	Lys	Tyr	Gly	Phe	Val	Gly	Arg	Lys	His	
	Leu	Leu	Ile	Phe	Asn	Leu	Ser	Asp	Gly	Asp	Ser	Gly	Val	Tyr	Gln	Cys	
5	Leu	Ser	Glu	Glu	Arg	Val	Arg	Asn	Lys	Thr	Val	Ser	Gln	Leu	Leu	Ala	
	Lys	His	Val	Leu	Glu	Val	Lys	Met	Val	Pro	Arg	Thr	Pro	Pro	Ser	Pro	
	Thr	Ser	Glu	Asp	Val	Gln	Thr	Glu	Gly	Ser	Lys	Ile	Thr	Ser	Lys	Met	
10																	
	Pro	Val	Gly	Ser	Thr	Gln	Gly	Ser	Ser	Pro	Pro	Thr	Pro	Ala	Leu	Trp	
	Ala	Thr	Ser	Pro	Arg	Ala	Ala	Thr	Leu	Pro	Pro	Lys	Ser	Ser	Ser	Gly	
15	Thr	Ser	Cys	Glu	Pro	Lys	Met	Val	Ile	Asn	Thr	Val	Pro	Gln	Leu	His	
	Ser	Glu	Lys	Thr	Val	Tyr	Leu	Lys	Ser	Ser	Asp	Asn	Arg	Leu	Leu	Met	
	Ser	Leu	Leu	Leu	Phe	Ile	Phe	Val	Leu	Phe	Leu	Cys	Leu	Phe	Ser	Tyr	
20																	
	Asn	Cys	Tyr	Lys	Gly	Tyr	Leu	Pro	Gly	Gln	Cys	Leu	Lys	Phe	Arg	Ser	
	Ala	Leu	Leu	Leu	Gly	Lys	Lys	Thr	Pro	Lys	Ser	Asp	Phe	Ser	Asp	Leu	
25	Glu	Gln	Ser	Val	Lys	Glu	Thr	Leu	Val	Glu	Pro	Gly	Ser	Phe	Ser	Gln	
	Gln	Asn	Gly	Asp	His	Pro	Lys	Pro	Ala	Leu	Asp	Thr	Gly	Tyr	Glu	Thr	
	Glu	Gln	Asp	Thr	Ile	Thr	Ser	Lys	Val	Pro	Thr	Asp	Arg	Glu	Asp	Ser	

	820	825	830
	Gln Arg Ile Asp Glu Leu Ser Ala Arg Asp Lys Pro Phe Asp Val Lys		
	835	840	845
	Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp		
5	850	855	860

<210> 2
 <211> 2769
 <212> DNA
 <213> Mouse

10 <400> 2

```

gaattcggca cgaggccatc catgtgtgcc cgttgctgaa ggcctcggtg gcccctgccc 60
atgaggatgt gtgcccccg tagggggctg ttcttggccc tggtagtagt gttgagaacc 120
gcggtggcat ttgcacctgt gcctcggctc acctgggaac atggagaggt aggtctggtg 180
cagtttcaca agccaggcat ctttaactac tcggccttgc tgatgagtga ggacaaagac 240
15 actctgtatg taggcgcccc ggaagcagtc ttgacagtga atgcgctgaa catctctgag 300
aagcaacatg aggtatatg gaaggtctct gaagacaaaa aatccaagtg tgcagagaag 360
gggaaatcaa agcagacgga atgcctaaac tacattcgag tactacagcc actaagcagc 420
acttcctct atgtgtgtgg gaccaatgcg ttccagccca cctgtgacca cctgaacttg 480
acatccttca agtttctggg gaaaagtga gatggcaaag gaagatgccc cttcgacccc 540
20 gcccacagct acacatcagt catggttggg ggcgagctct actctgggac gtcctataat 600
ttcttgggca gtgaacccat catctctcga aactcttccc acagtccctt gaggacggag 660
tatgccatcc cgtggctgaa cgagcctagc ttctgtcttg ctgacgtgat ccagaaaagc 720
ccagatggtc cggagggtga agatgacaag gtctacttct tttttacgga ggtatccgtg 780
gagtacgaat tcgtcttcaa gttgatgat cgcgagttg ccagggtgtg caagggcgac 840
25 cagggcggcc tgcggacttt gcaaaaaaag tggacctcct tcctaaaggc caggctgatc 900
tgctccaagc cagacagtgg cctggctctt aacatacttc aggatgtgtt tgtgtctagg 960
gccccgggcc tcaaggagcc tgtgttctat gcggtcttca ccccacagct gaacaatgtg 1020
ggctctgtcag cgggtgtgcg ctacacactg gccacggtgg aggcagtctt ctcccgtgga 1080
aagtacatgc agagtgccac agtggagcag tctcacacca agtgggtgcg ctacaatggc 1140

```

ccagtgccca ctccccgacc tggagcgtgt atcgacagtg aggcccgggc agccaactac 1200
 accagtcctt tgaatctccc agacaaaaca ctgcagtttg taaaagacca cccittgatg 1260
 gatgactcag tgaccccgat agacaacaga cccaagctga tcaaaaaaga tgtaaaactac 1320
 acccagatag tggtagacag gacccaggcc ctggatggga ctttctacga cgtcatgttc 1380
 5 atcagcacag accggggagc tctgcataaa gcagtcattc tcacaaaaga ggtgcatgtc 1440
 atcagaggaga cccaactctt ccgggacctt gaaccgggtc taactctgct gctatcgica 1500
 aagaagggga ggaagtttgt ctatgcaggc tccaactctg gagtgggtcca agcgcccctg 1560
 gcattctgcg aaaagcacgg tagctgtgaa gactgtgtgt tagcacggga cccctactgt 1620
 gcctggagcc cagccatcaa ggctgtgtt accctgcacc aggaagaggc ctccagcagg 1680
 10 ggctggattc aggacatgag cggtagacaca tcctcatgcc tggataagag taaagaaagt 1740
 ttcaaccagc attttttcaa gcacggcggc acagcggaac tcaaagtgtt caaaagtcc 1800
 aacctagccc ggggtggtatg gaagtccag aatggcgagt tgaaggccgc aagtcccaag 1860
 tacggctttg tgggcaggaa gcacctgctc atcttcaacc tgtcggacgg agacagcggc 1920
 gtgtaccagt gcctgtcaga ggaaaggggtg aggaataaaa cggctctcca gctgctggcc 1980
 15 aagcacgttc tggaagtga gatggtacct cggaccccc cctcacctac ctacagaggat 2040
 gttcagacag aaggtagtaa gatcacatcc aaaatgccgg ttggatctac ccaggggtcc 2100
 tctcccccta ccccggtctt gtgggcaacc tccccagag ccgccacct acctcccaag 2160
 tcctctccg gcacatctg tgaaccaaag atggatca acacgggtccc ccagctccac 2220
 tcagagaaga cgggtgtatc caagtccagt gacaaccgcc tgtcatgtc tctctctc 2280
 20 ttcatctttg tctcttctt ctgctcttt tctacaact gctacaaggg ctacctgccc 2340
 ggacagtgt taaaattccg ctacgccctg ctgcttgga agaaaacacc caagtcagac 2400
 ttctctgacc tggagcagag tgtgaaggag acactgggtc agcctgggag cttctcccag 2460
 cagaacggcg accaccccaa gccagccctg gatacgggt atgaaacgga gcaggacacc 2520
 atcaccagca aagtccccc ggatcgtgag gactcgcaac ggatcgatga actctctgcc 2580
 25 cgggacaaac cgtttgatgt caagtgtgaa ctgaagttg cagattcgga tgcigacggg 2640
 gactgaggcc agcgtgtccc agcccatgcc cctctgtctt cgtggagagt gttgtgttga 2700
 gccattcag tagccgagtc ttgtcactct gtgccagcct cagtcctgtg tccccitttt 2760
 ctctggttt 2769

<211> 862

<212> PRT

<213> Human

<400> 3

```

5  Met Arg Met Cys Thr Pro Ile Arg Gly Leu Leu Met Ala Leu Ala Val
    1             5             10             15
Met Phe Gly Thr Ala Met Ala Phe Ala Pro Ile Pro Arg Ile Thr Trp
    20             25             30
Glu His Arg Glu Val His Leu Val Gln Phe His Glu Pro Asp Ile Tyr
10             35             40             45
Asn Tyr Ser Ala Leu Leu Leu Ser Glu Asp Lys Asp Thr Leu Tyr Ile
    50             55             60
Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu
    65             70             75             80
15  Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ala Lys
    85             90             95
Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile
    100            105            110
Arg Val Leu Gln Pro Leu Ser Ala Thr Ser Leu Tyr Val Cys Gly Thr
20             115            120            125
Asn Ala Phe Gln Pro Ala Cys Asp His Leu Asn Leu Thr Ser Phe Lys
    130            135            140
Phe Leu Gly Lys Asn Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro
    145            150            155            160
25  Ala His Ser Tyr Thr Ser Val Met Val Asp Gly Glu Leu Tyr Ser Gly
    165            170            175
Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
    180            185            190
Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu

```

	195	200	205
	Pro Ser Phe Val Phe Ala Asp Val Ile Arg Lys Ser Pro Asp Ser Pro		
	210	215	220
	Asp Gly Glu Asp Asp Arg Val Tyr Phe Phe Phe Thr Glu Val Ser Val		
5	225	230	235 240
	Glu Tyr Glu Phe Val Phe Arg Val Leu Ile Pro Arg Ile Ala Arg Val		
	245	250	255
	Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr		
	260	265	270
10	Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Arg Pro Asp Ser Gly Leu		
	275	280	285
	Val Phe Asn Val Leu Arg Asp Val Phe Val Leu Arg Ser Pro Gly Leu		
	290	295	300
	Lys Val Pro Val Phe Tyr Ala Leu Phe Thr Pro Gln Leu Asn Asn Val		
15	305	310	315 320
	Gly Leu Ser Ala Val Cys Ala Tyr Asn Leu Ser Thr Ala Glu Glu Val		
	325	330	335
	Phe Ser His Gly Lys Tyr Met Gln Ser Thr Thr Val Glu Gln Ser His		
	340	345	350
20	Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Lys Pro Arg Pro Gly		
	355	360	365
	Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu		
	370	375	380
	Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met		
25	385	390	395 400
	Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Arg Leu Ile Lys Lys		
	405	410	415
	Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp		
	420	425	430

Gly Thr Val Tyr Asp Val Met Phe Val Ser Thr Asp Arg Gly Ala Leu
 435 440 445
 His Lys Ala Ile Ser Leu Glu His Ala Val His Ile Ile Glu Glu Thr
 450 455 460
 5 Gln Leu Phe Gln Asp Phe Glu Pro Val Gln Thr Leu Leu Leu Ser Ser
 465 470 475 480
 Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val
 485 490 495
 Gln Ala Pro Leu Ala Phe Cys Gly Lys His Gly Thr Cys Glu Asp Cys
 10 500 505 510
 Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Pro Thr Ala Thr
 515 520 525
 Cys Val Ala Leu His Gln Thr Glu Ser Pro Ser Arg Gly Leu Ile Gln
 530 535 540
 15 Glu Met Ser Gly Asp Ala Ser Val Cys Pro Asp Lys Ser Lys Gly Ser
 545 550 555 560
 Tyr Arg Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys
 565 570 575
 Ser Gln Lys Ser Asn Leu Ala Arg Val Phe Trp Lys Phe Gln Asn Gly
 20 580 585 590
 Val Leu Lys Ala Glu Ser Pro Lys Tyr Gly Leu Met Gly Arg Lys Asn
 595 600 605
 Leu Leu Ile Phe Asn Leu Ser Glu Gly Asp Ser Gly Val Tyr Gln Cys
 610 615 620
 25 Leu Ser Glu Glu Arg Val Lys Asn Lys Thr Val Phe Gln Val Val Ala
 625 630 635 640
 Lys His Val Leu Glu Val Lys Val Val Pro Lys Pro Val Val Ala Pro
 645 650 655
 Thr Leu Ser Val Val Gln Thr Glu Gly Ser Arg Ile Ala Thr Lys Val

	660	665	670
	Leu Val Ala Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Val Gln		
	675	680	685
	Ala Thr Ser Ser Gly Ala Ile Thr Leu Pro Pro Lys Pro Ala Pro Thr		
5	690	695	700
	Gly Thr Ser Cys Glu Pro Lys Ile Val Ile Asn Thr Val Pro Gln Leu		
	705	710	715
	His Ser Glu Lys Thr Met Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu		
	725	730	735
10	Met Ser Leu Phe Leu Phe Phe Phe Val Leu Phe Leu Cys Leu Phe Phe		
	740	745	750
	Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu Lys Phe Arg		
	755	760	765
	Ser Ala Leu Leu Ile Gly Lys Lys Lys Pro Lys Ser Asp Phe Cys Asp		
15	770	775	780
	Arg Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser		
	785	790	795
	Gln Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu		
	805	810	815
20	Thr Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp		
	820	825	830
	Ser Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val		
	835	840	845
	Lys Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp		
25	850	855	860

<210> 4

<211> 4157

<212> DNA

<213> Human

<400> 4

	ctgagccgca tctgcaatag cacacttgcc cggccacctg ctgccgtgag cctttgctgc	60
	tgaagcccct ggggtcgcct ctacctgatg aggatgtgca ccccattag ggggtgctc	120
	atggcccttg cagtgatgtt tgggacagcg atggcatttg caccataacc ccggtacc	180
5	tgggagcaca gagaggigca cctgggtgag ttcatgagc cagacatcta caactactca	240
	gccttgctgc tgagcgagga caaggacacc ttgtacatag gtgcccggga ggcgtcttc	300
	gctgtgaacg cactcaacat ctccgagaag cagcatgagg tgtattggaa ggtctcagaa	360
	gacaaaaaag caaatgtgc agaaaagggg aaatcaaac agacagagtg cctcaactac	420
	atccgggtgc tgcagccact cagcgccact tccctttacg tgtgtgggac caacgcattc	480
10	cagccggcct gtgaccacct gaacttaaca tcccttaagt ttctggggaa aaatgaagat	540
	ggcaaaggaa gatgtccctt tgaccagca cacagctaca catccgtcat ggttgatgga	600
	gaactttatt cggggacgtc gtataatttt ttgggaagtg aacccatcat ctccgaaat	660
	tcttcccaca gtctctgag gacagaatat gcaatccctt ggctgaacga gcctagtttc	720
	gtgtttgctg acgtgatccg aaaaagccca gacagccccg acggcgagga tgacagggtc	780
15	tactttctct tcacggaggt gtctgtggag tatgagtttg tgttcagggt gctgatccca	840
	cggatagcaa gagtgtgcaa gggggaccag ggcggcctga ggacctgca gaagaaatgg	900
	acctccttcc tgaaagcccg actcatctgc tcccggccag acagcggctt ggtcttcaat	960
	gtgctgcggg atgtcttcgt gctcagggtc ccgggcctga aggtgcctgt gttctatgca	1020
	ctcttcaccc cacagctgaa caacgtgggg ctgtcggcag tgtgcgccta caacctgtcc	1080
20	acagccgagg aggtcttctc ccacgggaag tacatgcaga gcaccacagt ggagcagtcc	1140
	cacaccaagt ggggtgcgcta taatggcccc gtaccaagc cgcggcctgg agcgtgcac	1200
	gacagcgagg cacgggccgc caactacacc agctccttga atttgccaga caagacgtg	1260
	cagttcgtaa aagaccaccc ttgatggat gactcggtaa ccccaataga caacaggccc	1320
	aggtaataca agaaagatgt gaactacacc cagatcgttg tggaccggac ccaggccctg	1380
25	gatgggactg tctatgatgt catgtttgtc agcacagacc ggggagctct gcacaaagcc	1440
	atcagcctcg agcacgtgt tcacatcatc gaggagaccc agctcttcca ggactttgag	1500
	ccagtccaga cctgtctgt gtcttcaaag aagggaaca ggittgtcta tgctggctct	1560
	aactcgggcg tgggtccaggc cccgtggcc ttctgtggga agcacggcac ctgcaggac	1620
	tgtgtgctgg cgcgggaccc ctactgcgcc tggagccgc ccacagcgac ctgcgtggct	1680

ctgcaccaga ccgagagccc cagcaggggt ttgattcagg agatgagcgg cgatgcttct 1740
 gtgtgcccgg ataaaagtaa aggaagttaac cggcagcatt ttttcaagca cggtaggcaca 1800
 gcggaactga aatgctccca aaaatccaac ctggcccggg tcttttggaa gticcagaat 1860
 ggcgtgttga aggccgagag cccaagtac ggtcttatgg gcagaaaaaa ctigtctatc 1920
 5 tccaacttgt cagaaggaga cagtgggggtg taccagtgcc tgtcagagga gagggttaag 1980
 aacaaaacgg tcttccaagt ggtcgccaag cagtccttgg aagtgaagggt ggttccaaag 2040
 cccgtagtgg cccccacctt gtcagttgtt cagacagaag gtagtaggat tgccaccaa 2100
 gtgttgggtg catccacca agggcttctt cccccaaccc cagccgtgca ggccacctcc 2160
 tccggggcca tcaccttcc tccaagcct gcgccaccg gcacatcctg cgaaccaaag 2220
 10 atcgtcatca acacgggtccc ccagctccac tcggagaaaa ccatgtatct taagtccagc 2280
 gacaaccgcc tctcatgtc cctcttctc tttcttttg ttctcttct ctgcctcttt 2340
 ttctacaact gctataaggg atacctgcc agacagtgt tgaattccg ctcgcccta 2400
 ctaattggga agaagaagcc caagtcagat ttctgtgacc gtgagcagag cctgaaggag 2460
 acgttagtag agccaggag cttctcccag cagaatgggg agcaccccaa gccagccctg 2520
 15 gacaccggct atgagaccga gcaagacacc atcaccagca aagtcccac ggataggag 2580
 gactcacaga ggatcgacga ctttctgcc agggacaagc ctttgacgt caagtgtgag 2640
 ctgaagtgc ctgactcaga cgcagatgga gactgaggcc ggctgtgcat ccccgctgg 2700
 gcctcggtg cgacgtgtc aggcgtggag agttttgtgt ttctcctgtt cagtatcca 2760
 gtctcgtgca gtgtgcgtg ggtagcccg catcgtgcag acaacctcag tctcttgtc 2820
 20 tattttctct tgggttgagc ctgtgacttg gtttctctt gtccttttgg aaaaatgaca 2880
 agcattgcat cccagctctt gtgtccgaag tcagtcggag tacttgaaga agggccacgg 2940
 gcggcacgga gtacctgagc ctttctgtg gtgggggaaa ggtggctgga cctctgttgg 3000
 ctgagaagag catcccttca gttccctc cccgtagcag ccactaaaag attattta 3060
 tccagattgg aaatgacatt ttagttatc agattggtaa cttatgcct gttgtccaga 3120
 25 ttggcacgaa cttttctt cacttaatta ttttttagg attttgctt gattgtgtt 3180
 atgtcatggg tcaTTTTTT ttagttacag aagcagttgt gttaatattt agaagaagat 3240
 gtatatctt cagattttgt tatatatgt gcataaata cggcttacgt tgcttaagat 3300
 tctcagggat aaacttctt ttgctaaatg cattcttct gcttttagaa atgtagacat 3360
 aaacacitcc cggagcccac tcacctttt tcttttctt tttttttt taactttatt 3420

ccttgaggga agcattgttt ttggagagat tttctttctg tacttcgttt tacttttctt 3480
 tttttttaac ttttactctc tcgaagaaga ggaccttccc acatccacga ggtgggtttt 3540
 gagcaaggga aggtagcctg gatgagctga gtggagccag gctggcccag agctgagatg 3600
 ggagtgcggt acaatctgga gcccacagct gtcggtcaga acctcctgtg agacagatgg 3660
 5 aaccttcaca agggcgccct tggttctctg aacatctcct ttctcttctt gcttcaattg 3720
 cttaccact gcctgcccag actttctatc cagcctcact gagctgccc ctactggaag 3780
 ggaactgggc ctcgggtggc ggggccgca gctgtgacca cagcacctc aagcatacgg 3840
 cgctgttcct gccactgtcc tgaagatgtg aatgggtggt acgatttcaa cactggttaa 3900
 tttcacactc catctccccg ctttgtaaat acccatcggg aagagacttt ttttccatgg 3960
 10 tgaagagcaa taaactctgg atgtttgtgc gcgtgtgtgg acagtcttat cttccagcat 4020
 gataggattt gaccattttg gtgtaaacad ttgtgtttta taagatttac cttgttttta 4080
 ttttctact ttgaattgta tacatttgga aagtacccaa ataaatgaga agcttctatc 4140
 cttaaaaaaa aaaaaaa 4157

<210> 5

15 <211> 361

<212> PRT

<213> Mouse

<400> 5

20	Met	Ala	Asp	Ala	Ile	Thr	Tyr	Ala	Asp	Leu	Arg	Phe	Val	Lys	Val	Pro
					5					10					15	
	Leu	Lys	Asn	Ser	Ala	Ser	Asn	His	Leu	Gly	Gln	Asp	Cys	Glu	Ala	Tyr
					20					25					30	
	Glu	Asp	Gly	Glu	Leu	Thr	Tyr	Glu	Asn	Val	Gln	Val	Ser	Pro	Val	Pro
					35					40					45	
25	Gly	Gly	Pro	Pro	Gly	Leu	Ala	Ser	Pro	Ala	Leu	Ala	Asp	Lys	Ala	Gly
					50					55					60	
	Val	Gly	Ser	Glu	Gln	Pro	Thr	Ala	Thr	Trp	Ser	Ser	Val	Asn	Ser	Ser
					65					70					75	80
	Ala	Leu	Arg	Gln	Ile	Pro	Arg	Cys	Pro	Thr	Val	Cys	Leu	Gln	Tyr	Phe

		85		90		95	
	Leu	Leu	Gly	Leu	Leu	Val	Ser
				Cys	Leu	Met	Leu
					Gly	Val	Ala
						Val	Ile
		100		105		110	
	Cys	Leu	Gly	Val	Arg	Tyr	Leu
				Gln	Val	Ser	Arg
					Gln	Phe	Gln
					Glu	Gly	
5		115		120		125	
	Thr	Arg	Ile	Trp	Glu	Ala	Thr
				Asn	Ser	Ser	Leu
					Gln	Gln	Gln
					Leu	Arg	
		130		135		140	
	Glu	Lys	Ile	Ser	Gln	Leu	Gly
				Gln	Lys	Glu	Val
					Glu	Val	Glu
					Leu	Gln	Lys
					Ala		
	145			150		155	
							160
10	Arg	Lys	Glu	Leu	Ile	Ser	Ser
				Gln	Asp	Thr	Leu
					Gln	Glu	Lys
					Gln	Arg	
				165		170	
							175
	Thr	His	Glu	Asp	Ala	Glu	Gln
				Gln	Gln	Leu	Gln
					Ala	Cys	Gln
					Ala	Glu	Arg
				180		185	
							190
	Ala	Lys	Thr	Lys	Glu	Asn	Leu
				Lys	Thr	Glu	Glu
					Glu	Glu	Arg
					Arg	Arg	Arg
					Asp		
15				195		200	
							205
	Leu	Asp	Gln	Arg	Leu	Thr	Ser
				Thr	Arg	Glu	Thr
					Leu	Arg	Arg
					Phe	Phe	
				210		215	
							220
	Ser	Asp	Ser	Ser	Asp	Thr	Cys
				Cys	Pro	Cys	Gly
					Trp	Ile	Pro
					Tyr	Gln	
				225		230	
							235
							240
20	Glu	Arg	Cys	Phe	Tyr	Ile	Ser
				His	Thr	Leu	Gly
					Ser	Leu	Glu
					Glu	Ser	
				245		250	
							255
	Gln	Lys	Tyr	Cys	Thr	Ser	Leu
				Ser	Ser	Lys	Leu
					Ala	Ala	Phe
					Asp	Glu	
				260		265	
							270
	Pro	Ser	Lys	Tyr	Tyr	Tyr	Glu
				Tyr	Leu	Ser	Asp
					Ala	Pro	Gln
					Val	Ser	
25				275		280	
							285
	Leu	Pro	Ser	Gly	Leu	Glu	Glu
				Leu	Leu	Asp	Arg
					Ser	Lys	Ser
					Tyr	Trp	
				290		295	
							300
	Ile	Gln	Met	Ser	Lys	Lys	Trp
				Arg	Gln	Asp	Ser
					Asp	Ser	Gln
					Ser	Arg	
				305		310	
							315
							320

His Cys Val Arg Ile Lys Thr Tyr Tyr Gln Lys Trp Glu Arg Thr Ile

325

330

335

Ser Lys Cys Ala Glu Leu His Pro Cys Ile Cys Glu Ser Glu Ala Phe

340

345

350

5 Arg Phe Pro Asp Gly Ile Asn Leu Asn

355

360

<210> 6

<211> 1357

<212> DNA

10 <213> Mouse

<400> 6

tggaagactg tgaagcagag gcgcccaggg ctatggctga cgctatcacg tatgcagacc 60

tgcgcttttgt gaaagtgtccc ctgaagaaca gcgcatctaa ccatctagga caggactgtg 120

aggcctatga agatggggaa ctcacctacg agaatgtgca agtgtctcca gtcccaggag 180

15 ggccaccagg cttggcttcc cctgcactag cggacaaagc aggggtcggg tcagagcaac 240

caactgcgac ctggagctct gtgaactcgt ctgctctcag gcagattccc cgctgtccta 300

cagtctgctt gcaatacttc ttgcttggcc ttctcgtgtc ctgtctgatg ttaggggtgg 360

ctgtcatctg cctgggagtt cgctatctgc aggtgtctcg gcagttccag gaggggacca 420

ggatttggga agccaccaat agcagcctgc agcagcagct cagggagaag ataagtcagc 480

20 tggggcagaa ggagggtggag cttcagaagg ctcggaagaa gctgatctcg agccaggaca 540

cattacagga gaagcagagg actcacgagg acgctgagca gcaactacaa gcctgccagg 600

ctgagagagc gaagaccaag gagaacctga aaactgagga ggagcggagg agggacctgg 660

accagaggtt gacaagcacg cgggagacac tgaggcgctt cttctctgat tcatcagaca 720

cctgctgtcc atgcggatgg attccatata aggaaagggtg cttttacata tcacataccc 780

25 tcggaagtct ggaggagagc caaaaatact gcacatctct gtcctccaaa ctggcagcat 840

tcgatgaacc ttctaagtat tactatgaag ttctctgtcc cagcggctta gaggagtgc 900

tagatcgttc gaagtcatat tggatacaga tgagcaagaa gtggaggcag gactctgact 960

ctcaaagccg acattgtgtc aggataaaaa catattacca gaagtgggaa agaacaattt 1020

ccaagtgtgc agagcttcac ccttgcatit gtgagtcgga ggctttcagg tttctgatg 1080

ggatcaatct gaactgaaac ggacacttga acaagacctt gtgacctaca tccttaacct 1140
 acggcctgcc aatttttaag actgctattc ctccagcact ccctcactct cgggcatgcc 1200
 cagctaaggg atgacctgct gcttgcttga aagctgctcc agaaactigga ctctctcttgg 1260
 gaagagtaaa gaagcctcca gaaaagacctt gaccttcctt aagaacttcc caaactagag 1340
 5 atgggtcagg ggagggc 1357
 <210> 7
 <211> 359
 <212> PRT
 <213> Human
 10 <400> 7
 Met Ala Glu Ala Ile Thr Tyr Ala Asp Leu Arg Phe Val Lys Ala Pro
 5 10 15
 Leu Lys Lys Ser Ile Ser Ser Arg Leu Gly Gln Asp Pro Gly Ala Asp
 20 25 30
 15 Asp Asp Gly Glu Ile Thr Tyr Glu Asn Val Gln Val Pro Ala Val Leu
 35 40 45
 Gly Val Pro Ser Ser Leu Ala Ser Ser Val Leu Gly Asp Lys Ala Ala
 50 55 60
 Val Lys Ser Glu Gln Pro Thr Ala Ser Trp Arg Ala Val Thr Ser Pro
 20 65 70 75 80
 Ala Val Gly Arg Ile Leu Pro Cys Arg Thr Thr Cys Leu Arg Tyr Leu
 85 90 95
 Leu Leu Gly Leu Leu Leu Thr Cys Leu Leu Leu Gly Val Thr Ala Ile
 100 105 110
 25 Cys Leu Gly Val Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr
 115 120 125
 Asn Arg Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg
 130 135 140
 Leu Lys Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser

145						150						155						160
Arg	Arg	Glu	Leu	Ala	Gln	Ser	Gln	Glu	Ala	Leu	Gln	Val	Glu	Gln	Arg			
					165						170						175	
Ala	His	Gln	Ala	Ala	Glu	Gly	Gln	Leu	Gln	Ala	Cys	Gln	Ala	Asp	Arg			
					180						185						190	
Gln	Lys	Thr	Lys	Glu	Thr	Leu	Gln	Ser	Glu	Glu	Gln	Gln	Arg	Arg	Ala			
					195						200						205	
Leu	Glu	Gln	Lys	Leu	Ser	Asn	Met	Glu	Asn	Arg	Leu	Lys	Pro	Phe	Phe			
					210						215						220	
Thr	Cys	Gly	Ser	Ala	Asp	Thr	Cys	Cys	Pro	Ser	Gly	Trp	Ile	Met	His			
					225						230						240	
Gln	Lys	Ser	Cys	Phe	Tyr	Ile	Ser	Leu	Thr	Ser	Lys	Asn	Trp	Gln	Glu			
					245						250						255	
Ser	Gln	Lys	Gln	Cys	Glu	Thr	Leu	Ser	Ser	Lys	Leu	Ala	Thr	Phe	Ser			
					260						265						270	
Glu	Ile	Tyr	Pro	Gln	Ser	His	Ser	Tyr	Tyr	Phe	Leu	Asn	Ser	Leu	Leu			
					275						280						285	
Pro	Asn	Gly	Gly	Ser	Gly	Asn	Ser	Tyr	Trp	Thr	Gly	Leu	Ser	Ser	Asn			
					290						295						300	
Lys	Asp	Trp	Lys	Leu	Thr	Asp	Asp	Thr	Gln	Arg	Thr	Arg	Thr	Tyr	Ala			
					305						310						320	
Gln	Ser	Ser	Lys	Cys	Asn	Lys	Val	His	Lys	Thr	Trp	Ser	Trp	Trp	Thr			
					325						330						335	
Leu	Glu	Ser	Glu	Ser	Cys	Arg	Ser	Ser	Leu	Pro	Tyr	Ile	Cys	Glu	Met			
					340						345						350	
Thr	Ala	Phe	Arg	Phe	Pro	Asp												
					355						359							

$\langle 210 \rangle$ 8

<211> 1531

<212> DNA

<213> Human

<400> 8

```

    agtcacagag ggaacacaga gcctagtgtt aaacggacag agacgagagg ggcaagggag   60
5   gacagtggat gacaggggaag acgagtgggg gcagagctgc tcaggaccat ggctgaggcc  120
    atcacctatg cagatctgag gtttgtgaag gctcccctga agaagagcat ctccagccgg  180
    ttaggacagg acccaggggc tgaatgatgat ggggaaatca cctacgagaa tgttcaagtg  240
    cccgcagtcc taggggtgcc ctcaagcttg gcttcttctg tactagggga caaagcagcg  300
    gtcaagtcgg agcagccaac tgcgtccttg agagccgtga cgtcaccagc tgtcgggcgg  360
10  attctccctt gccgcacaac ctgcctgcga tacctcctgc tcggcctgct cctcacctgc  420
    ctgctgttag gagtgaccgc catctgcctg ggagtgcgt atctgcaggt gtctcagcag  480
    ctccagcaga cgaacagggt tctggaagtc actaacagca gcctgaggca gcagctccgc  540
    ctcaagataa cgcagctggg acagagtgcg gaggatctgc aggggtccag gagagagctg  600
    gcgcagagtc aggaagcact acaggtggaa cagagggctc atcaggcggc cgaagggcag  660
15  ctacaggcct gccaggcaga cagacagaag acgaaggaga ccttgcaaag tgaggagcaa  720
    cagaggaggg ccttggagca gaagctgagc aacatggaga acagactgaa gcccttcttc  780
    acatgcggct cagcagacac ctgctgtccg tcgggatgga taatgcatca gaaaagctgc  840
    ttttacatct cacttacttc aaaaaatttg caggagagcc aaaaacaatg tgaaactctg  900
    tcttccaagc tggccacatt cagtgaat tttccacaat cacactctta ctacttctta  960
20  aattcactgt tgccaaatgg tggttcaggg aattcatatt ggactggcct cagctctaac 1020
    aaggattgga agttgactga tgatacaca cgcactagga cttatgctca aagctcaaaa 1080
    tgtaacaagg tacataaaac ttggtcatgg tggacactgg agtcagagtc atgtagaagt 1140
    tctcttccct acatctgtga gatgacagct ttcaggtttc cagattagga cagtcctttg 1200
    cactgagttg aactcatgc caacaagaac ctgtgcccct ccttccctaac ctgaggcctg 1260
25  gggttcctca gaccatctcc ttcatcttgg gcagtgccag ccaccggctg acccacacct 1320
    gacacttcca gccagtctgc tgcctgtccc ctcttctga aactggactg ttcttgggaa 1380
    aagggtgaag ccacctctag aagggaactt ggctccccc caagaacttc ccatggtaga 1440
    atgggggtggg ggaggagggc gcacgggctg agcggatagg ggcggcccgg agccagccag 1500
    gcagttttat tgaaatcttt ttaaataatt g                                     1531

```

<210> 9

<211> 32

<212> DNA

<213> Artificial Sequence

5 <220>

<223>

<400> 9

gctgtcgact gtgtgcccgt tgctgaaggc ct

32

<210> 10

10 <211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223>

15 <400> 10

gacggatcct acttactttg ctttgcttgc ttgagataca ccgtcttctc tga

53